Docket No.: 066661-0017 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

re Application of	:	Customer Number: 41552
Goodlett, David R., et al.	:	Confirmation Number: 3333
Serial No.: 09/748,783	:	Group Art Unit: 1631
Filed: December 26, 2000	:	Examiner: Mahatan Channing

For: RAPID AND QUANTITATIVE PROTEOME ANALYSIS AND RELATED METHODS

Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

DECLARATION PURSUANT TO 37 C.F.R. § 1.132

I, David R. Goodlett, declare as follows:

1) I am the David R. Goodlett who is an inventor of the above-identified application.

2) I understand that the claims stand rejected as allegedly obvious over Yates, J. Mass Spectrom. 33:1-19 (1998), alone or in combination with Gygi et al., Nat. Biotechnol. 17:994-999 (1999), or Easterling et al., Anal. Chem. 71:624-632 (1999).

3) The methods described by Yates are distinct from the claimed methods. Yates is a review article describing mass spectrometry and how it is used in the study of proteomics. Yates describes typical usage of mass spectrometry for proteomics analysis. Peptides are generated in solution, generally using enzymatic digestion. The enzymatically generated peptides are analyzed by mass spectrometry using one of two approaches. One approach is to measure the masses of the enzymatically generated peptides without further fragmentation in the mass spectrometer, that is, so called mass mapping or fingerprinting. A

second approach is to select one of the enzymatically generated peptides, fragment the selected peptide in the mass spectrometer, and measure the mass of the fragment ions, that is, so called tandem mass spectrometry or MS/MS.

4) As recited in claim 1, the mass of parent polypeptides (such as enzymatically generated peptides) are measured simultaneously with the mass of fragments. This is distinct from the description in Yates of measuring the masses of the parent polypeptides without further fragmentation in the mass spectrometer.

5) In claims 13, 24 and 56, the claims specifically recite that fragment mass is determined by mass spectrometry in the absence of ion selection for producing fragment ions. This is distinct from the description in Yates of selecting a single parent polypeptide, fragmenting the selected peptide in the mass spectrometer, and measuring the masses of fragment ions.

6) In conclusion, I believe that the claimed methods are distinct from the two historical mass spectrometry methods reviewed by Yates.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that any such willful false statement may jeopardize the validity of the application or any patent issued thereon.

13 July 2004

Date

Signature David R. Goodlett, Ph.D.